

FIGURE 1

10 20 30 40 50 60 70
 GTCGACTCTA GAGTGTGTGT CAGCACTTGG CTGGGGACTT CTTGAACTTG CAGGGAGAAT AACTTGC GCA

80 90 100 110 120 130 140
 CCCCACCTTTG CGCCGGTGCC TTTGCCCCAG CGGAGCCTGC TTCGCCATCT CCGAGCCCCA CCGCCCCTCC

150 160 170 180 190 200 210
 ACTCCTCGGC CTTGCCCGAC ACTGAGACGC TGTTC CAGC GTGAAAAGAG AGACTGCGCG GCCGGCACCC

220 230 240 250 260 270 280
 GGGAGAAGGA GGAGGCAAAG AAAAGGAACG GACATTCGGT CCTTGCGCCA GGTCTTTGA CCAGAGTTTT

290 300 310 320 330 340 350
 TCCATGTGGA CGCTCTTTCA ATGGACGTGT CCCC GCGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT

(1) 370 385 400
 CGACC ATG GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC
 MET Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val

415 430 445
 CTC CTG GGC GGC GCG GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC GCG
 Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe Ala
 (24)

460 475 490 505
 GCG GCG TCG TCG GGC CGC CCC TCA TCC CAG CCC TCT GAC GAG GTC CTG AGC GAG
 Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val Leu Ser Glu

520 535 550 565
 TTC GAG TTG CGG CTG CTC AGC ATG TTC GGC CTG AAA CAG AGA CCC ACC CCC AGC
 Phe Glu Leu Arg Leu Leu Ser MET Phe Gly Leu Lys Gln Arg Pro Thr Pro Ser

580 595 610
 AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC CTG TAT CGC AGG CAC TCA GGT
 Arg Asp Ala Val Val Pro Pro Tyr MET Leu Asp Leu Tyr Arg Arg His Ser Gly

625 640 655 670
 CAG CCG GGC TCA CCC GCC CCA GAC CAC CGG TTG GAG AGG GCA GCC AGC CGA GCC
 Gln Pro Gly Ser Pro Ala Pro Asp His Arg Leu Glu Arg Ala Ala Ser Arg Ala

FIGURE 1 (CON'T)

FIGURE 1 (CON'T)

1330					1345					1360					1375																			
TTT	TAC	TGC	CAC	GGA	GAA	TGC	CCT	TTT	CCT	CTG	GCT	GAT	CAT	CTG	AAC	TCC	ACT																	
Phe	Tyr	Cys	His	Gly	Glu	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser	Thr																	
1390					1405					1420																								
AAT	CAT	GCC	ATT	GTT	CAG	ACG	TTG	GTC	AAC	TCT	GTT	AAC	TCT	AAG	ATT	CCT	AAG																	
Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Lys	Ile	Pro	Lys																	
1435					1450					1465					1480																			
GCA	TGC	TGT	GTC	CCG	ACA	GAA	CTC	AGT	GCT	ATC	TCG	ATG	CTG	TAC	CTT	GAC	GAG																	
Ala	Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	MET	Leu	Tyr	Leu	Asp	Glu																	
1495					1510					1525																								
AAT	GAA	AAG	GTT	GTA	TTA	AAG	AAC	TAT	CAG	GAC	ATG	GTT	GTG	GAG	GGT	TGT	GGG																	
Asn	Glu	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Asp	MET	Val	Val	Glu	Gly	Cys	Gly																	
1540(396)					1553					1563					1573					1583					1593					1603				
TGT	CGC	TAG	TAC	AGCA	AAATTA	AAATA	CATAA	TATA	TATATATATA	TATATATATA	TATATTTTAG	AAAAA	AAGAAA																					
Cys	Arg																																	

AAAA

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FIGURE 2

10 20 30 40 50 60 70
 CTCTAGAGGG CAGAGGAGGA GGGAGGGAGG GAAGGAGCGC GGAGCCCGGC CCGGAAGCTA GGTGAGTGTG
 80 90 100 110 120 130 140
 GCATCCGAGC TGAGGGACGC GAGCCTGAGA CGCCGCTGCT GCTCCGGCTG AGTATCTAGC TTGTCTCCCC
 150 160 170 180 190 200 210
 GATGGGATTC CCGTCCAAGC TATCTCGAGC CTGCAGCGCC ACAGTCCCCG GCCCTCGCCC AGGTTCACTG
 220 230 240 250 260 270 280
 CAACCGTTCA GAGGTCCCCA GGAGCTGCTG CTGGCGAGCC CGCTACTGCA GGGACCTATG GAGCCATTCC
 290 300 310 320 330 340 350
 GTAGTGCCAT CCCGAGCAAC GCACTGCTGC AGCTTCCCTG AGCCTTTCCA GCAAGTTTGT TCAAGATTGG
 360 370 380 390 400 (1)
 CTGTCAAGAA TCATGGACTG TTATTATATG CCTTGTTTTT TGTCAAGACA CC ATG ATT CCT
 MET Ile Pro
 417 432 447 462
 GGT AAC CGA ATG CTG ATG GTC GTT TTA TTA TGC CAA GTC CTG CTA GGA GGC GCG
 Gly Asn Arg MET Leu MET Val Val Leu Leu Cys Gln Val Leu Leu Gly Gly Ala
 477 492 507
 AGC CAT GCT AGT TTG ATA CCT GAG ACG GGG AAG AAA AAA GTC GCC GAG ATT CAG
 Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys Lys Lys Val Ala Glu Ile Gln
 522 537 552 567
 GGC CAC GCG GGA GGA CGC CGC TCA GGG CAG AGC CAT GAG CTC CTG CGG GAC TTC
 Gly His Ala Gly Gly Arg Arg Ser Gly Gln Ser His Glu Leu Leu Arg Asp Phe
 582 597 612 627
 GAG GCG ACA CTT CTG CAG ATG TTT GGG CTG CGC CGC CGC CCG CAG CCT AGC AAG
 Glu Ala Thr Leu Leu Gln MET Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys
 642 657 672
 AGT GCC GTC ATT CCG GAC TAC ATG CGG GAT CTT TAC CGG CTT CAG TCT GGG GAG
 Ser Ala Val Ile Pro Asp Tyr MET Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu

FIGURE 2 (CON'T)

687	702	717	732
GAG GAG GAA GAG CAG ATC CAC AGC ACT GGT CTT GAG TAT CCT GAG CGC CCG GCC			
Glu Glu Glu Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala			
747	762	777	
AGC CGG GCC AAC ACC GTG AGG AGC TTC CAC CAC GAA GAA CAT CTG GAG AAC ATC			
Ser Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn Ile			
792	807	822	837
CCA GGG ACC AGT GAA AAC TCT GCT TTT CGT TTC CTC TTT AAC CTC AGC AGC ATC			
Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu Ser Ser Ile			
852	867	882	897
CCT GAG AAC GAG GTG ATC TCC TCT GCA GAG CTT CGG CTC TTC CGG GAG CAG GTG			
Pro Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu Phe Arg Glu Gln Val			
912	927	942	
GAC CAG GGC CCT GAT TGG GAA AGG GGC TTC CAC CGT ATA AAC ATT TAT GAG GTT			
Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His Arg Ile Asn Ile Tyr Glu Val			
957	972	987	1002
ATG AAG CCC CCA GCA GAA GTG GTG CCT GGG CAC CTC ATC ACA CGA CTA CTG GAC			
MET Lys Pro Pro Ala Glu Val Val Pro Gly His Leu Ile Thr Arg Leu Leu Asp			
1017	1032	1047	
ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG GAA ACT TTT GAT GTG AGC CCT			
Thr Arg Leu Val His His Asn Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro			
1062	1077	1092	1107
GCG GTC CTT CGC TGG ACC CGG GAG AAG CAG CCA AAC TAT GGG CTA GCC ATT GAG			
Ala Val Leu Arg Trp Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu			
1122	1137	1152	1167
GTG ACT CAC CTC CAT CAG ACT CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC			
Val Thr His Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser			
1182	1197	1212	
CGA TCG TTA CCT CAA GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC			
Arg Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val			
1227	1242	1257	1272
ACC TTT GGC CAT GAT GGC CGG GGC CAT GCC TTG ACC CGA CGC CGG AGG GCC AAG			
Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg Arg Ala Lys			
1287	1302	1317	
CGT AGC CCT AAG CAT CAC TCA CAG CGG GCC AGG AAG AAG AAT AAG AAC TGC CGG			
Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys Arg			

(293)

FIGURE 2 (CON'T)

1332 1347 1362 1377
 CGC CAC TCG CTC TAT GTG GAC TTC AGC GAT GTG GGC TGG AAT GAC TGG ATT GTG
 Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val

 1392 1407 1422 1437
 GCC CCA CCA GGC TAC CAG GCC TTC TAC TGC CAT GGG GAC TGC CCC TTT CCA CTG
 Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp Cys Pro Phe Pro Leu

 1452 1467 1482
 GCT GAC CAC CTC AAC TCA ACC AAC CAT GCC ATT GTG CAG ACC CTG GTC AAT TCT
 Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser

 1497 1512 1527 1542
 GTC AAT TCC AGT ATC CCC AAA GCC TGT TGT GTG CCC ACT GAA CTG AGT GCC ATC
 Val Asn Ser Ser Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile

 1557 1572 1587
 TCC ATG CTG TAC CTG GAT GAG TAT GAT AAG GTG GTA CTG AAA AAT TAT CAG GAG
 Ser MET Leu Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu

1602 1617 (408) 1636 1646 1656
 ATG GTA GTA GAG GGA TGT GGG TGC CGC TGAGATCAGG CAGTCCTTGA GGATAGACAG
MET Val Val Glu Gly Cys Gly Cys Arg

 1666 1676 1686 1696 1706 1716 1726
 ATATACACAC CACACACACA CACCACATAC ACCACACACA CACGTTCCCA TCCACTCACC CACACACTAC

 1736 1746 1756 1766 1776 1786 1796
 ACAGACTGCT TCCTTATAGC TGGACTTTTA TTTAAAAAAA AAAAAAAAAA AATGGAAAAA ATCCCTAAAC

 1806 1816 1826 1836 1846 1856 1866
 ATTCACCTTG ACCTTATTTA TGACTTTACG TGCAAATGTT TTGACCATAT TGATCATATA TTTTGACAAA

 1876 1886 1896 1906 1916 1926 1936
 ATATATTTAT AACTACGTAT TAAAAGAAAA AAATAAAATG AGTCATTATT TTAAAAAAA AAAAAAACT

 1946
 CTAGAGTCGA CGGAATTC

FIGURE 3

10 20 30 40 50
 GTGACCGAGC GGCGCGGACG GCCGCCTGCC CCCTCTGCCA CCTGGGGCGG

60 70 80 90 99
 TGC GGGCCCCG GAGCCCGGAG CCCGGGTAGC GCGTAGAGCC GGCGCG ATG
 MET
 (1)

108	117	126	135	144
CAC GTG CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG				
His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala				
153	162	171	180	189
CTC TGG GCA CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC				
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe				
198	207	216	225	234
AGC CTG GAC AAC GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC				
Ser Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu				
243	252	261	270	279
CGC AGC CAG GAG CGG CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT				
Arg Ser Gln Glu Arg Arg Glu MET Gln Arg Glu Ile Leu Ser Ile				
288	297	306	315	324
TTG GGC TTG CCC CAC CGC CCG CGC CCG CAC CTC CAG GGC AAG CAC				
Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His				
333	342	351	360	369
AAC TCG GCA CCC ATG TTC ATG CTG GAC CTG TAC AAC GCC ATG GCG				
Asn Ser Ala Pro MET Phe MET Leu Asp Leu Tyr Asn Ala MET Ala				
378	387	396	405	414
GTG GAG GAG GGC GGC GGG CCC GGC GGC CAG GGC TTC TCC TAC CCC				
Val Glu Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro				
423	432	441	450	459
TAC AAG GCC GTC TTC AGT ACC CAG GGC CCC CCT CTG GCC AGC CTG				
Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu				
468	477	486	495	504
CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC ATG GTC ATG AGC TTC				
Gln Asp Ser His Phe Leu Thr Asp Ala Asp MET Val MET Ser Phe				
513	522	531	540	549
GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC CAC CCA CGC TAC				
Val Asn Leu Val Glu His Asp Lys Glu Phe Phe His Pro Arg Tyr				

FIGURE 3 (Con't)

CAC	CAT	558	GAG	TTC	567	CGG	TTT	GAT	CTT	576	TCC	AAG	ATC	CCA	585	GAA	594	GGG
His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	Pro	Glu	Gly				
GAA	GCT	603	GTC	ACG	GCA	612	GCC	GAA	TTC	621	CGG	ATC	TAC	AAG	630	GAC	639	ATC
Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	Tyr	Ile				
CGG	GAA	648	CGC	TTC	GAC	657	AAT	GAG	ACG	666	TTC	CGG	ATC	AGC	675	GTT	684	CAG
Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile	Ser	Val	Tyr	Gln				
GTG	CTC	693	CAG	GAG	CAC	702	TTG	GGC	AGG	711	GAA	TCG	GAT	CTC	720	TTC	729	CTC
Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu				
GAC	AGC	738	CGT	ACC	CTC	747	TGG	GCC	TCG	756	GAG	GAG	GGC	TGG	765	CTG	774	TTT
Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe				
GAC	ATC	783	ACA	GCC	ACC	792	AGC	AAC	CAC	801	TGG	GTG	GTC	AAT	810	CCG	819	CAC
Asp	Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His				
AAC	CTG	828	GGC	CTG	CAG	837	CTC	TCG	GTG	846	GAG	ACG	CTG	GAT	855	GGG	864	AGC
Asn	Leu	Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser				
ATC	AAC	873	CCC	AAG	TTG	882	GCG	GGC	CTG	891	ATT	GGG	CGG	CAC	900	GGG	909	CAG
Ile	Asn	Pro	Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln				
AAC	AAG	918	CAG	CCC	TTC	927	ATG	GTG	GCT	936	TTC	TTC	AAG	GCC	945	ACG	954	GTC
Asn	Lys	Gln	Pro	Phe	MET	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val				
CAC	TTC	963	CGC	AGC	ATC	972	CGG	TCC	ACG	981	GGG	AGC	AAA	CAG	990	CGC	999	CAG
His	Phe	Arg	Ser	Ile	Arg	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln				
(293)																		
AAC	CGC	1008	TCC	AAG	ACG	1017	CCC	AAG	AAC	1026	CAG	GAA	GCC	CTG	1035	CGG	1044	ATG
Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	Gln	Glu	Ala	Leu	Arg	MET	Ala				
AAC	GTG	1053	GCA	GAG	AAC	1062	AGC	AGC	AGC	1071	GAC	CAG	AGG	CAG	1080	GCC	1089	TGT
Asn	Val	Ala	Glu	Asn	Ser	Ser	Ser	Ser	Asp	Gln	Arg	Gln	Ala	Cys	Lys			

FIGURE 3 (Con't)

1098	1107	1116	1125	1134
AAG CAC GAG CTG TAT GTC AGC TTC CGA GAC CTG GGC TGG CAG GAC				
Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp				
1143	1152	1161	1170	1179
TGG ATC ATC GCG CCT GAA GGC TAC GCC GCC TAC TAC TGT GAG GGG				
Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly				
1188	1197	1206	1215	1224
GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC ACC AAC CAC				
Glu Cys Ala Phe Pro Leu Asn Ser Tyr MET Asn Ala Thr Asn His				
1233	1242	1251	1260	1269
GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC CCG GAA ACG GTG				
Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Ile Ser Val				
1278	1287	1296	1305	1314
CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC ATC TCC GTC				
Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val				
1323	1332	1341	1350	1359
CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA TAC AGA				
Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg				
1368	1377	1386	1399	
AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC				
Asn MET Val Val Arg Ala Cys Gly Cys His				
		(431)		
1409	1419	1429	1439	1448
GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTC				

Figure 4

10 20 30 40 50
 CGACCATGAG AGATAAGGAC TGAGGGCCAG GAAGGGGAAG CGAGCCCGCC
 60 70 80 90 100
 GAGAGGTGGC GGGGACTGCT CACGCCAAGG GCCACAGCGG CCGCGCTCCG
 110 120 130 140 150
 GCCTCGCTCC GCCGCTCCAC GCCTCGCGGG ATCCGCGGGG GCAGCCCGGC
 159 168 177 186 195
 CGGGCGGGG ATG CCG GGG CTG GGG CGG AGG GCG CAG TGG CTG TGC
 MET Pro Gly Leu Gly Arg Arg Ala Gln Trp Leu Cys
 (1)
 204 213 222 231 240
 TGG TGG TGG GGG CTG CTG TGC AGC TGC TGC GGG CCC CCG CCG CTG
 Trp Trp Trp Gly Leu Leu Cys Ser Cys Cys Gly Pro Pro Pro Leu
 249 258 267 276 285
 CGG CCG CCC TTG CCC GCT GCC GCG GCC GCC GCC GCC GGG GGG CAG
 Arg Pro Pro Leu Pro Ala Ala Ala Ala Ala Ala Ala Gly Gly Gln
 294 303 312 321 330
 CTG CTG GGG GAC GGC GGG AGC CCC GGC CGC ACG GAG CAG CCG CCG
 Leu Leu Gly Asp Gly Gly Ser Pro Gly Arg Thr Glu Gln Pro Pro
 339 348 357 366 375
 CCG TCG CCG CAG TCC TCC TCG GGC TTC CTG TAC CGG CGG CTC AAG
 Pro Ser Pro Gln Ser Ser Ser Gly Phe Leu Tyr Arg Arg Leu Lys
 384 393 402 411 420
 ACG CAG GAG AAG CGG GAG ATG CAG AAG GAG ATC TTG TCG GTG CTG
 Thr Gln Glu Lys Arg Glu MET Gln Lys Glu Ile Leu Ser Val Leu
 429 438 447 456 465
 GGG CTC CCG CAC CGG CCC CGG CCC CTG CAC GGC CTC CAA CAG CCG
 Gly Leu Pro His Arg Pro Arg Pro Leu His Gly Leu Gln Gln Pro

Figure 4 (Con't)

CAG	CCC	474	CGG	GCG	CTC	483	CAG	CAG	492	GAG	CAG	501	CAG	CAG	510	CAG	
Gln	Pro	Pro	Pro	Ala	Leu	Arg	Gln	Gln	Glu	Glu	Gln	Gln	Gln	Gln	Gln	Gln	
CAG	CTG	519	CCT	CGC	GGA	528	GAG	CCC	537	GGG	CGA	546	CTG	AAG	TCC	555	GCG
Gln	Leu	Pro	Arg	Arg	Gly	Glu	Pro	Pro	Pro	Gly	Arg	Leu	Lys	Ser	Ser	Ala	Ala
CCC	CTC	564	TTC	ATG	CTG	573	GAT	CTG	582	AAC	GCC	591	TCC	GCC	GAC	600	AAC
Pro	Leu	Phe	MET	Leu	Asp	Leu	Tyr	Asn	Ala	Leu	Ser	Ala	Ala	Asp	Asn	Asn	Asn
GAC	GAG	609	GAC	GGG	GCG	618	TCG	GAG	627	GGG	GAG	636	CAG	TCC	TGG	645	CCC
Asp	Glu	Asp	Asp	Gly	Ala	Ser	Glu	Gly	Glu	Arg	Gln	Gln	Ser	Trp	Pro	Pro	Pro
CAC	GAA	654	GCA	GCC	AGC	663	TCG	TCC	672	CGT	CGG	681	CAG	CCG	CCC	690	GGC
His	Glu	Ala	Ala	Ala	Ser	Ser	Ser	Gln	Arg	Arg	Gln	Pro	Pro	Pro	Gly	Ser	Ser
GCC	GCG	699	CAC	CCG	CTC	708	AAC	CGC	717	AGC	CTT	726	CTG	GCC	CCC	735	GGA
Pro	Pro	Gly	Ala	Ala	Ala	His	Pro	Leu	Asn	Arg	Lys	Ser	Leu	Leu	Ala	Ala	TCT
GGC	AGC	744	GGC	GGC	GCG	753	TCC	CCA	762	ACC	AGC	771	GCG	CAG	GAC	780	AGC
Gly	Ser	Gly	Gly	Gly	Ala	Ser	Pro	Leu	Thr	Ser	Ala	Gln	Asp	Ser	Ala	Ala	GCC
TTC	CTC	789	AAC	GAC	GCG	798	GAC	ATG	807	GTC	ATG	816	TTT	GTG	AAC	825	CTG
Phe	Leu	Asn	Asp	Ala	Ala	Asp	MET	Val	MET	Ser	Phe	Val	Val	Asn	Leu	Val	GTG
GAG	TAC	834	GAC	AAG	GAG	843	TTC	TCC	852	CGT	CAG	861	CGA	CAC	CAC	870	AAA
Glu	Tyr	Asp	Asp	Lys	Glu	Phe	Ser	Pro	Arg	Gln	Arg	His	His	Lys	Glu	Glu	GAG
TTC	AAG	879	TTC	AAC	TTA	888	TCC	CAG	897	CCT	GAG	906	GGT	GAG	GTG	915	GTG
Phe	Lys	Phe	Asn	Leu	Leu	Ser	Gln	Ile	Pro	Glu	Gly	Glu	Val	Val	Val	Thr	ACG
GCT	GCA	924	GAA	TTC	CGC	933	ATC	TAC	942	GAC	TGT	951	GTT	ATG	GGG	960	AGT
Phe	Arg	Ile	Tyr	Lys	Lys	Asp	Cys	Val	MET	Ala	Ala	Glu	Gly	Ser	Phe	Phe	TTT

Figure 4 (Con't)

969	978	987	996	1005
AAA AAC CAA ACT TTT CTT ATC AGC ATT TAT CAA GTC TTA CAG GAG				
Lys Asn Gln Thr Phe Leu Ile Ser Ile Tyr Gln Val Leu Gln Glu				
1014	1023	1032	1041	1050
CAT CAG CAC AGA GAC TCT GAC CTG TTT TTG TTG GAC ACC CGT GTA				
His Gln His Arg Asp Ser Asp Leu Phe Leu Leu Asp Thr Arg Val				
1059	1068	1077	1086	1095
GTA TGG GCC TCA GAA GAA GGC TGG CTG GAA TTT GAC ATC ACG GCC				
Val Trp Ala Ser Glu Glu Gly Trp Leu Glu Phe Asp Ile Thr Ala				
1104	1113	1122	1131	1140
ACT AGC AAT CTG TGG GTT GTG ACT CCA CAG CAT AAC ATG GGG CTT				
Thr Ser Asn Leu Trp Val Val Thr Pro Gln His Asn MET Gly Leu				
1149	1158	1167	1176	1185
CAG CTG AGC GTG GTG ACA AGG GAT GGA GTC CAC GTC CAC CCC CGA				
Gln Leu Ser Val Val Thr Arg Asp Gly Val His Val His Pro Arg				
1194	1203	1212	1221	1230
GCC GCA GGC CTG GTG GGC AGA GAC GGC CCT TAC GAT AAG CAG CCC				
Ala Ala Gly Leu Val Gly Arg Asp Gly Pro Tyr Asp Lys Gln Pro				
1239	1248	1257	1266	1275
TTC ATG GTG GCT TTC TTC AAA GTG AGT GAG GTC CAC GTG CGC ACC				
Phe MET Val Ala Phe Phe Lys Val Ser Glu Val His Val Arg Thr				
1284	1293	1302	1311	1320
ACC AGG TCA GCC TCC AGC CGG CGC CGA CAA CAG AGT CGT AAT CGC				
Thr Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser Arg Asn Arg				
(382)				
1329	1338	1347	1356	1365
TCT ACC CAG TCC CAG GAC GTG GCG CGG GTC TCC AGT GCT TCA GAT				
<u>Ser Thr Gln Ser Gln Asp Val Ala Arg</u> Val Ser Ser Ala Ser Asp				
(388)				
1374	1383	1392	1401	1410
TAC AAC AGC AGT GAA TTG AAA ACA GCC TGC AGG AAG CAT GAG CTG				
Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys <u>His Glu Leu</u>				
(412)				
1419	1428	1437	1446	1455
TAT GTG AGT TTC CAA GAC CTG GGA TGG CAG GAC TGG ATC ATT GCA				
<u>Tyr Val Ser Phe</u> Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala				

Figure 4 (Con't)

1464	1473	1482	1491	1500
CCC AAG GGC TAT GCT GCC AAT TAC TGT GAT GGA GAA TGC TCC TTC				
Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe				
1509	1518	1527	1536	1545
CCA CTC AAC GCA CAC ATG AAT GCA ACC AAC CAC GCG ATT GTG CAG				
Pro Leu Asn Ala His MET Asn Ala Thr Asn His Ala Ile Val Gln				
1554	1563	1572	1581	1590
ACC TTG GTT CAC CTT ATG AAC CCC GAG TAT GTC CCC AAA CCG TGC				
Thr Leu Val His Leu MET Asn Pro Glu Tyr Val Pro Lys Pro Cys				
1599	1608	1617	1626	1635
TGT GCG CCA ACT AAG CTA AAT GCC ATC TCG GTT CTT TAC TTT GAT				
Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp				
1644	1653	1662	1671	1680
GAC AAC TCC AAT GTC ATT CTG AAA AAA TAC AGG AAT ATG GTT GTA				
Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn MET Val Val				
1689	1698	1708	1718	1728
AGA GCT TGT GGA TGC CAC TAACTCGAAA CCAGATGCTG GGGACACACA				
Arg Ala Cys Gly Cys His				
(513)				
1738	1748	1758	1768	1778
TTCTGCCTTG GATTCCTAGA TTACATCTGC CTTAAAAAAA CACGGAAGCA				
1788	1798	1808	1818	1828
CAGTTGGAGG TGGGACGATG AGACTTTGAA ACTATCTCAT GCCAGTGCCT				
1838	1848	1858	1868	1878
TATTACCCAG GAAGATTTTA AAGGACCTCA TTAATAATTT GCTCACTTGG				
1888	1898	1908	1918	1928
TAAATGACGT GAGTAGTTGT TGGTCTGTAG CAAGCTGAGT TTGGATGTCT				
1938	1948	1958	1968	1978
GTAGCATAAG GTCTGGTAAC TGCAGAAACA TAACCGTGAA GCTCTTCCTA				
1988	1998	2008	2018	2028
CCCTCCTCCC CCAAAAACCC ACCAAAATTA GTTTTAGCTG TAGATCAAGC				
2038	2048	2058	2068	2078
TATTTGGGGT GTTTGTTAGT AAATAGGGAA AATAATCTCA AAGGAGTTAA				
2088	2098	2108	2118	2128
ATGTATTCTT GGCTAAAGGA TCAGCTGGTT CAGTACTGTC TATCAAAGGT				

Figure 4 (Con't)

2138	2148	2158	2168	2178
AGATTTTACA	GAGAACAGAA	ATCGGGGAAG	TGGGGGGAAC	GCCTCTGTTC
2188	2198	2208	2218	2228
AGTTCATTCC	CAGAAGTCCA	CAGGACGCAC	AGCCCAGGCC	ACAGCCAGGG
2238	2248	2258	2268	2278
CTCCACGGGG	CGCCCTTGTC	TCAGTCATTG	CTGTTGTATG	TTCGTGCTGG
2288	2298	2308	2318	2328
AGTTTTGTGTG	GTGTGAAAAT	ACACTTATTT	CAGCCAAAAC	ATACCATTTC
2338	2348	2358	2368	2378
TACACCTCAA	TCCTCCATTT	GCTGTACTCT	TTGCTAGTAC	CAAAAGTAGA
2388	2398	2408	2418	2428
CTGATTACAC	TGAGGTGAGG	CTACAAGGGG	TGTGTAACCG	TGTAACACGT
2438	2448	2458	2468	2478
GAAGGCAGTG	CTCACCTCTT	CTTTACCAGA	ACGGTTCCTT	GACCAGCACA
2488	2498	2508	2518	2528
TTAACTTCTG	GACTGCCGGC	TCTAGTACCT	TTTCAGTAAA	GTGGTTCTCT
2538	2548	2558	2568	2578
GCCTTTTTTAC	TATACAGCAT	ACCACGCCAC	AGGGTTAGAA	CCAACGAAGA
2588	2598	2608	2618	2628
AAATAAAATG	AGGGTGCCCA	GCTTATAAGA	ATGGTGTTAG	GGGGATGAGC
2638	2648	2658	2668	2678
ATGCTGTTTA	TGAACGGAAA	TCATGATTTT	CCTGTAGAAA	GTGAGGCTCA
2688	2698	2708	2718	2728
GATTAAATTT	TAGAATATTT	TCTAAATGTC	TTTTTCACAA	TCATGTGACT
2738	2748	2758	2768	2778
GGAAGGCAA	TTTCATACTA	AACTGATTAA	ATAATACATT	TATAATCTAC
2788	2798	2808	2818	2828
AACTGTTTGC	ACTTACAGCT	TTTTTTGTAA	ATATAAACTA	TAATTTATTG
2838	2848	2858	2868	2878
TCTATTTTAT	ATCTGTTTTG	CTGTGGCGTT	GGGGGGGGGG	CCGGGCTTTT
2888	2898	2908	2918	
GGGGGGGGGG	GTTTGTGTTG	GGGGTGTCGT	GGTGTGGGCG	GGCGG

Figure 5

10	20	30	40	50
CTGGTATATT	TGTGCCTGCT	GGAGGTGGAA	TTAACAGTAA	GAAGGAGAAA
60	70	80	90	100
GGGATTGAAT	GGACTTACAG	GAAGGATTTT	AAGTAAATTC	AGGGAAACAC
110	120	130	140	150
ATTTACTTGA	ATAGTACAAC	CTAGAGTATT	ATTTTACACT	AAGACGACAC
160	170	180	190	200
AAAAGATGTT	AAAGTTATCA	CCAAGCTGCC	GGACAGATAT	ATATTCCAAC
210	220	230	240	250
ACCAAGGTGC	AGATCAGCAT	AGATCTGTGA	TTCAGAAATC	AGGATTTGTT
260	270	280	290	300
TTGGAAAGAG	CTCAAGGGTT	GAGAAGAACT	CAAAAGCAAG	TGAAGATTAC
310	320	330	340	350
TTTGGGAACT	ACAGTTTATC	AGAAGATCAA	CTTTTGCTAA	TTCAAATACC
360	370	380	390	400
AAAGGCCTGA	TTATCATAAA	TTCATATAGG	AATGCATAGG	TCATCTGATC
410	420	430	440	450
AAATAATATT	AGCCGTCTTC	TGCTACATCA	ATGCAGCAAA	AACTCTTAAC
460	470	480	490	500
AACTGTGGAT	AATTGGAAAT	CTGAGTTTCA	GCTTTCTTAG	AAATAACTAC
510	520	530	540	550
TCTTGACATA	TTCCAAAATA	TTTAAAATAG	GACAGGAAAA	TCGGTGAGGA
560	570	580	590	600
TGTTGTGCTC	AGAAATGTCA	CTGTCATGAA	AAATAGGTAA	ATTTGTTTTT
610	620	630	640	650
TCAGCTACTG	GGAAACTGTA	CCTCCTAGAA	CCTTAGGTTT	TTTTTTTTTT
660	670	680	690	700
AAGAGGACAA	GAAGGACTAA	AAATATCAAC	TTTTGCTTTT	GGACAAAA

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Figure 5 (Con't)

701	710	719	728	737
ATG CAT CTG ACT GTA TTT TTA CTT AAG GGT ATT GTG GGT TTC CTC				
MET His Leu Thr Val Phe Leu Leu Lys Gly Ile Val Gly Phe Leu				
(1)				
746	755	764	773	782
TGG AGC TGC TGG GTT CTA GTG GGT TAT GCA AAA GGA GGT TTG GGA				
Trp Ser Cys Trp Val Leu Val Gly Tyr Ala Lys Gly Gly Leu Gly				
791	800	809	818	827
GAC AAT CAT GTT CAC TCC AGT TTT ATT TAT AGA AGA CTA CGG AAC				
Asp Asn His Val His Ser Ser Phe Ile Tyr Arg Arg Leu Arg Asn				
836	845	854	863	872
CAC GAA AGA CGG GAA ATA CAA AGG GAA ATT CTC TCT ATC TTG GGT				
His Glu Arg Arg Glu Ile Gln Arg Glu Ile Leu Ser Ile Leu Gly				
881	890	899	908	917
TTG CCT CAC AGA CCC AGA CCA TTT TCA CCT GGA AAA ATG ACC AAT				
Leu Pro His Arg Pro Arg Pro Phe Ser Pro Gly Lys Gln Ala Ser				
926	935	944	953	962
CAA GCG TCC TCT GCA CCT CTC TTT ATG CTG GAT CTC TAC AAT GCC				
Ser Ala Pro Leu Phe MET Leu Asp Leu Tyr Asn Ala MET Thr Asn				
971	980	989	998	1007
GAA GAA AAT CCT GAA GAG TCG GAG TAC TCA GTA AGG GCA TCC TTG				
Glu Glu Asn Pro Glu Glu Ser Glu Tyr Ser Val Arg Ala Ser Leu				
1016	1025	1034	1043	1052
GCA GAA GAG ACC AGA GGG GCA AGA AAG GGA TAC CCA GCC TCT CCC				
Ala Glu Glu Thr Arg Gly Ala Arg Lys Gly Tyr Pro Ala Ser Pro				
1061	1070	1079	1088	1097
AAT GGG TAT CCT CGT CGC ATA CAG TTA TCT CGG ACG ACT CCT CTG				
Asn Gly Tyr Pro Arg Arg Ile Gln Leu Ser Arg Thr Thr Pro Leu				
1106	1115	1124	1133	1142
ACC ACC CAG AGT CCT CCT CTA GCC AGC CTC CAT GAT ACC AAC TTT				
Thr Thr Gln Ser Pro Pro Leu Ala Ser Leu His Asp Thr Asn Phe				
1151	1160	1169	1178	1187
CTG AAT GAT GCT GAC ATG GTC ATG AGC TTT GTC AAC TTA GTT GAA				
Leu Asn Asp Ala Asp MET Val MET Ser Phe Val Asn Leu Val Glu				
1196	1205	1214	1223	1232
AGA GAC AAG GAT TTT TCT CAC CAG CGA AGG CAT TAC AAA GAA TTT				
Arg Asp Lys Asp Phe Ser His Gln Arg Arg His Tyr Lys Glu Phe				

Figure 5 (con't)

1241	1250	1259	1268	1277
CGA TTT GAT CTT ACC CAA ATT CCT CAT GGA GAG GCA GTG ACA GCA				
Arg Phe Asp Leu Thr Gln Ile Pro His Gly Glu Ala Val Thr Ala				
1286	1295	1304	1313	1322
GCT GAA TTC CGG ATA TAC AAG GAC CGG AGC AAC AAC CGA TTT GAA				
Ala Glu Phe Arg Ile Tyr Lys Asp Arg Ser Asn Asn Arg Phe Glu				
1331	1340	1349	1358	1367
AAT GAA ACA ATT AAG ATT AGC ATA TAT CAA ATC ATC AAG GAA TAC				
Asn Glu Thr Ile Lys Ile Ser Ile Tyr Gln Ile Ile Lys Glu Tyr				
1376	1385	1394	1403	1412
ACA AAT AGG GAT GCA GAT CTG TTC TTG TTA GAC ACA AGA AAG GCC				
Thr Asn Arg Asp Ala Asp Leu Phe Leu Leu Asp Thr Arg Lys Ala				
1421	1430	1439	1448	1457
CAA GCT TTA GAT GTG GGT TGG CTT GTC TTT GAT ATC ACT GTG ACC				
Gln Ala Leu Asp Val Gly Trp Leu Val Phe Asp Ile Thr Val Thr				
1466	1475	1484	1493	1502
AGC AAT CAT TGG GTG ATT AAT CCC CAG AAT AAT TTG GGC TTA CAG				
Ser Asn His Trp Val Ile Asn Pro Gln Asn Asn Leu Gly Leu Gln				
1511	1520	1529	1538	1547
CTC TGT GCA GAA ACA GGG GAT GGA CGC AGT ATC AAC GTA AAA TCT				
Leu Cys Ala Glu Thr Gly Asp Gly Arg Ser Ile Asn Val Lys Ser				
1556	1565	1574	1583	1592
GCT GGT CTT GTG GGA AGA CAG GGA CCT CAG TCA AAA CAA CCA TTC				
Ala Gly Leu Val Gly Arg Gln Gly Pro Gln Ser Lys Gln Pro Phe				
1601	1610	1619	1628	1637
ATG GTG GCC TTC TTC AAG GCG AGT GAG GTA CTT CTT CGA TCC GTG				
MET Val Ala Phe Phe Lys Ala Ser Glu Val Leu Leu Arg Ser Val				
1646	1655	1664	1673	1682
AGA GCA GCC AAC AAA CGA AAA AAT CAA AAC CGC AAT AAA TCC AGC				
Arg Ala Ala Asn Lys Arg Lys Asn Gln Asn Arg Asn Lys <u>Ser Ser</u>				
				(329)
1691	1700	1709	1718	1727
TCT CAT CAG GAC TCC TCC AGA ATG TCC AGT GTT GGA GAT TAT AAC				
<u>Ser His Gln Asp Ser Ser Arg</u> MET Ser Ser Val Gly Asp Tyr Asn				
				(337)

Figure 5 (Con't)

1736	1745	1754	1763	1772	
ACA AGT GAG CAA AAA CAA GCC TGT AAG AAG CAC GAA CTC TAT GTG					
Thr Ser Glu Gln Lys Gln Ala Cys Lys Lys <u>His Glu Leu Tyr Val</u>					
				(356)	
1781	1790	1799	1808	1817	
AGC TTC CGG GAT CTG GGA TGG CAG GAC TGG ATT ATA GCA CCA GAA					
<u>Ser Phe</u> Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu					
(362)					
1826	1835	1844	1853	1862	
GGA TAC GCT GCA TTT TAT TGT GAT GGA GAA TGT TCT TTT CCA CTT					
Gly Tyr Ala Ala Phe Tyr Cys Asp Gly Glu Cys Ser Phe Pro Leu					
1871	1880	1889	1898	1907	
AAC GCC CAT ATG AAT GCC ACC AAC CAC GCT ATA GTT CAG ACT CTG					
Asn Ala His MET Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu					
1916	1925	1934	1943	1952	
GTT CAT CTG ATG TTT CCT GAC CAC GTA CCA AAG CCT TGT TGT GCT					
Val His Leu MET Phe Pro Asp His Val Pro Lys Pro Cys Cys Ala					
1961	1970	1979	1988	1997	
CCA ACC AAA TTA AAT GCC ATC TCT GTT CTG TAC TTT GAT GAC AGC					
Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser					
2006	2015	2024	2033	2042	
TCC AAT GTC ATT TTG AAA AAA TAT AGA AAT ATG GTA GTA CGC TCA					
Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn MET Val Val Arg Ser					
2051	2060	2070	2080	2090	2100
TGT GGC TGC CAC TAATATTAAA TAATATTGAT AATAACAAAA AGATCTGTAT					
Cys Gly Cys His					
	(454)				
2110	2120	2130	2140	2150	
TAAGGTTTAT GGCTGCAATA AAAAGCATAC TTTCAGACAA ACAGAAAAAA AAA					

Figure 6

(1)
GAATTCC GAG CCC CAT TGG AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT
Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala
(10)

GGG GAG GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC
Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His
(20) (30)

CTG CTC AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC
Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser
(40) (50)

AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA GCT GGA GAC
Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala Gly Asp
(60) (70)

GAG GGC TGG CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC TGG TTG CTG AAG
Glu Gly Typ Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cyc Trp Leu Leu Lys
(80)

CGT CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG ACT GAG GAT GGG CAC AGC
Arg His Lys Asp Leu Gly Lue Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser
(90) (100)

GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT CAA CGG GCC CCA CGC TCC CAA CAG
Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln
(110) (120)

CCT TTC GTG GTC ACT TTC TTC AGG GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG
Pro Phe Val Val Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg
(130) (140)

GCA GTG AGG CCA CTG AGG AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG
Ala Val Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln
(150) (160)

GCC AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC CAC GGC CGG CAG
Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln
(170)

GTC TGC CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG GAC CTT GGC TGG CTG GAC
Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp
(180) (190)

TGG GTC ATC GCC CCC CAA GGC TAC TCA GCC TAT TAC TGT GAG GGG GAG TGC TCC
Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser
(200) (210)

TTC CCG CTG GAC TCC TGC ATG AAC GCC ACC AAC CAC GCC ATC CTG CAG TCC CTG
Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu
(220) (230)

Figure 6 (Con't)

GTG CAC CTG ATG AAG CCA AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC AAG
Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys
(240) (250)

CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC AGC AGC AAC AAC GTC ATC CTG CGC
Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg
(260)

AAG CAC CGC AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC TGAGTCAGCCCGCCCAGC
Lys His Arg Asn Met Val Val Lys Ala Cys Gly Cys His
(270) (280)

CCTACTGCAGCCACCCTTCTCATCTGGATCGGGCCCTGCAGAGGCAGAAAACCCTTAAATGCTGTCACAG
CTCAAGCAGGAGTGTCAGGGGCCCTCACTCTCGGTGCCTACTTCCTGTCAGGCTTCTGGGAATTC

FIGURE 7

GACGAAAGGG CCTCGTGATA CGOCTATTTT TATAGGTTAA TGTCATGATA ATAATGGTTT 60
 CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCOTATT TGTATTATTT 120
 TCTAAATACA TTCAATATG TATCGGCTCA TGAGACAATA ACCGTGATAA ATGCTTCAAT 180
 AATATTGAAA AAGGAGAGCT ATGAGTATTC AACATTTGCG TGTGCGCCTT ATTCCCTTTT 240
 TTGCGGGCATT TTGCCTTCCT GTTTTGTCTC ACCGAGAAAC GCTGGTGAAA GTAAAAGATG 300
 CTGAAGATCA GTTGGGTGCA CGAGTGGGT ACATCGAACT GGATCTCAAC AGCGGTAAAG 360
 TCCTTGAGAG TTTTCGCCCC GAGGAACTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC 420
 TATGTGGCGC GGTATTATCC CGTATTOACC CCGGGCAAGA GCAACTCGGT CGCGCGATAC 480
 ACTATTOTCA GAATGACTTG GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG 520
 GGATGACAGT AAGAGAATTA TGCAGTGTG GCATAACCAT GAGTGATAAC ACTGCGGCCA 600
 ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTGTG CACAACATGG 660
 GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAAAG 720
 ACGAGCGTGA CACCACGATG CCGTAGCAA TGGCAACAAC GTTGGCGAAA CTATTAAGTG 780
 GCGAACTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG 840
 TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG 900
 GAGCCCGTGA GCGTGGGTCT CCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAAGCGT 960
 CCGGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC 1020
 AGATCGGTGA GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTGAGAC CAAGTTTACT 1080
 CATATATACT TTAGATTGAT TTAAAAGTTC ATTTTARTT TAAAAGGATC TAGGTGAAGA 1140
 TCCTTTTGA TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTT CACTGAGCCT 1200
 CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTCCTG GCGTAATCT 1260
 GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGCT TTGTTTGGCG GATCAAGAGG 1320
 TACCAACTCT TTTCCGAAG GTAAGTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC 1380
 TTCTAGTGA GCCGTAGTTA GCGCACCACT TCAAGAACTC TGTAGCACCG COTACATACC 1440
 TCGCTCTGCT AATGCTGTTA CCACTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG 1500
 GGTGGACTC AAGACGATAG TTACCGGATA AAGCGCAGCG GTCGGGCTGA ACGGGGGGTT 1560
 CGTGACACA GCGGAGCTTG GAGCGAACGA COTACACCGA ACTGAGATAC CTACAGCGTG 1620
 AGCATTGAGA AAGCGCCAGC CTTCCGGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAAGC 1680
 GCAGCGTCG AACAGGAGAG GGCACGAGCG AGCTTCAGG GGGAAACGCC TGGTATCTTT 1740
 ATAGTCTGT CCGGTTTCGC CACCTCTGAC TTGAGCGTGG ATTTTGTGA TGCTCGTCAG 1800
 GGGGGCGGAG CCTATGAAA AACCGCAGCA ACGCGGCTT TTTACCGTTC CTGCGCTTTT 1860
 GCTGGCCTTT TGCTCACATG TTCTTCCTG CGTTATCCCC TGATTCTGTG GATAACCGTA 1920

FIGURE 7 (cont'd)

TTACGGCCTT TGAGTGAGCT GATACCGCTC GCGCGAGCGG AACGACCGAG CGCAGCGAGT 1980
 CAGTGAGCGA GGRAGCGGAA GAGCGGCCAA TACGCAAAAC GCCTCTCCCC GCGCGTTGGC 2040
 CGATTCAATTA ATGCAGAATT CATCTCTCAC CTACCAACA ATGCCCCCOT CCAAAAATA 2100
 AATTCAATATA AAAACATAC AGATAACCAT CTGCGGTGAT AAATTATCTC TGGCGGTGTT 2160
 GACATAAATA CCACTGGCGG TGATACTGAG CACATCAGCA GCACGCACTG ACCACCATGA 2220
 AGGTGACGCT CTTAAAAATT AAGCCCTGAA GAAGGCGAGC ATTCAAAGCA GAAGGCTTTG 2280
 GGGTGTGTGA TACGAACGA AGCATTGGCC GTAAGTCCGA TTCCGGATTA GCTGCCAATG 2340
 TGCCCAATGCG GGGGGGTTTT CGTTCAGGAC TACAACCTGCC ACACACCACC AAAGCTAACT 2400
 GACAGGAGAA TCCAGATGGA TGCACAAACA CCGCGCCGCG AACGTCCGCG AGAGAAACAG 2460
 GGTCAATGGA AAGCAGCAAA TCCCGTGTG GTTGGGGTAA GCGCAAAAC AGTTCCGAAA 2520
 GATTTTTTTA ACTATAAACG CTGATCGAAG CGTTTATGCG GAAGAGGTAA AGCCCTTCCC 2580
 GAGTAACAAA AAAACAACAG CATAAATAAC CCGCTCTTA CACATTCCAG CCCTGAAAAA 2640
 GGGCATCAAA TTAACCACA CCTATGGTGT ATGCATTAT TTGCATACAT TCAATCAATT 2700
 GTTATCTAAG GAATACTTA CATATGCAAG CTAACATAA ACAACGTAA CGTCTGAAT 2760
 CTAGCTGTAA GAGACACCCT TTGTACGTGG ACTTCAGTGA CGTGGGGTGG AATGACTGGA 2820
 TTGTGGCTCC CCGGGGTAT CACGCCCTTT ACTGCCACGG AGAATGCCCT TTTCCTCTGG 2880
 CTGATCATCT GAACCTCACT AATCATGCCA TTGTTCAAGC GTTGGTCAAC TCTGTTAACT 2940
 CTRAGATTCC TAAGGCATGC TGTGTCCGA CAGAAGTCAG TGCTATCTCG ATGCTGTACC 3000
 TTGACGAGAA TGAAAAGGTT GTATTAAAG ACTATCAGGA CATGGTTGTG GAGGTTGTG 3060
 GGTOTCGCTA GTACAGCAAA ATTAATACA TAATATATA TATATATATA TATTTAGAA 3120
 AAAAGAAAAA AATCTAGAGT CGACCTGCAG TAATCGTACA GGTAGTACA AATAAAAAAG 3180
 GCAOGTCAGA TGACGTCCCT TTTTCTTGT GAGCAGTAAG CTTGGCACTG GCGCTCGTTT 3240
 TACAACGTG TGACTGGGA AACCTGGCG TTACCAACT TAATCCCTT GCAGCACATC 3300
 CCCCTTTGCG CAGCTGGCGT AATAGCGAG AGGCCCGCAC CGATCGCCCT TCCCAACAGT 3360
 TGCGCAGCCT GAATGGCGAA TGGCGCCTGA TGCGGTATTT TCTCCTTACG CATCTGTGCG 3420
 GTATTTCACA CCGCATATAT GGTGCACTCT CAGTACAATC TGCTCTGATG CCGCATAGTT 3480
 AAGCCAGCCC CGACACCCGC CAACACCCGC TGACCGCCGC TGACGGGCTT GTCTGCTCCC 3540
 GGCATCCGCT TACAGACAAG CTGTGACCGT CTCGGGAGC TGCATGTGTC AGAGGTTTTT 3600
 ACCGTCAATCA CCGAAACCG CGA 3623

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FIGURE 8

W-20 ALKALINE PHOSPHATASE: BMP-2 vs. BMP-2/7

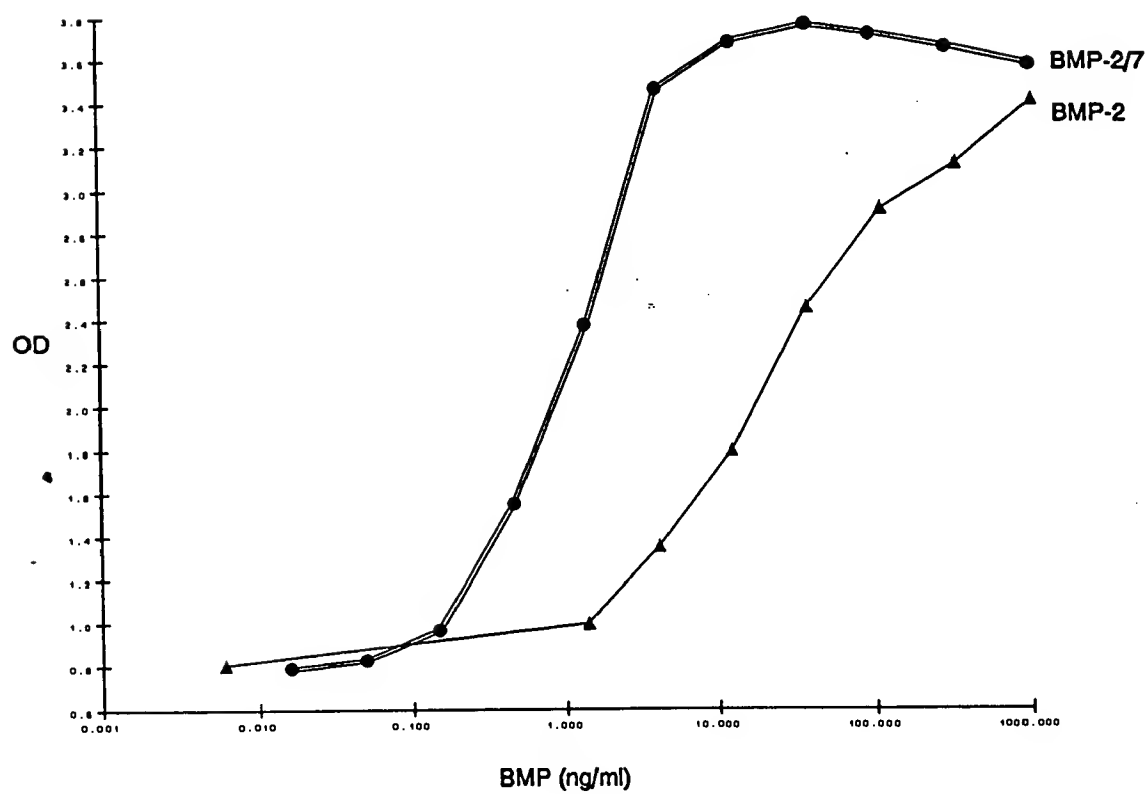


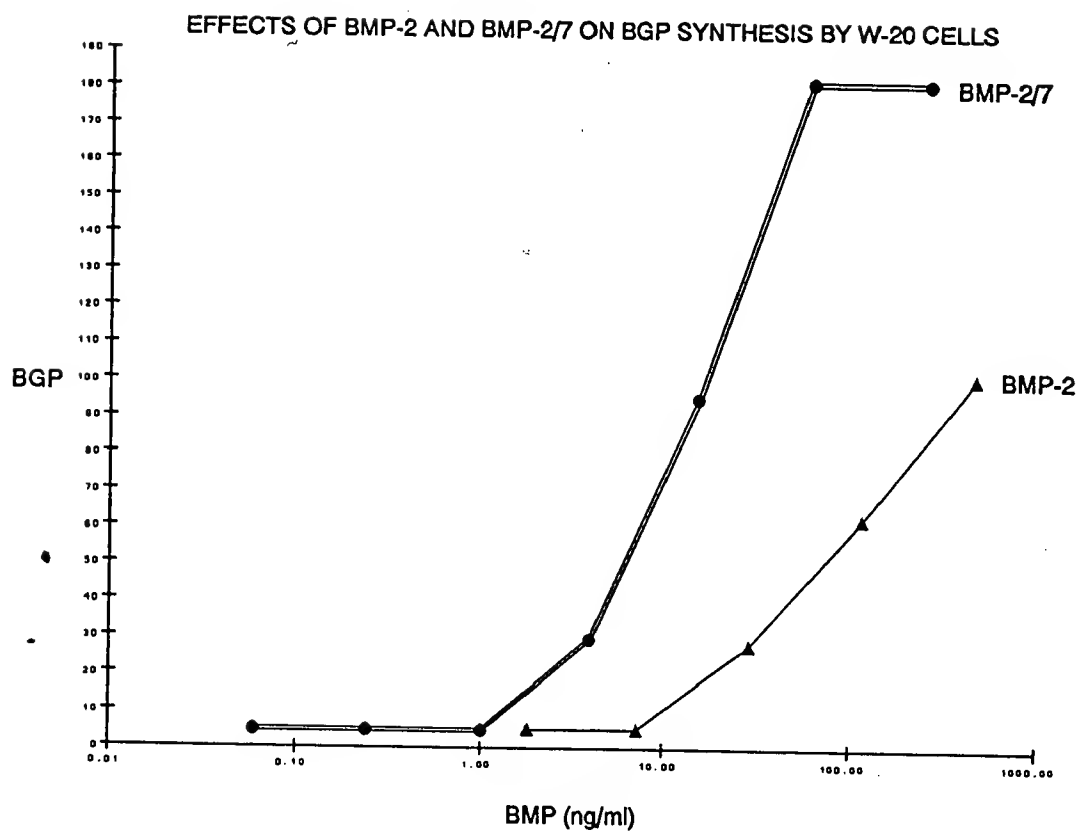
FIGURE 9

FIGURE 10

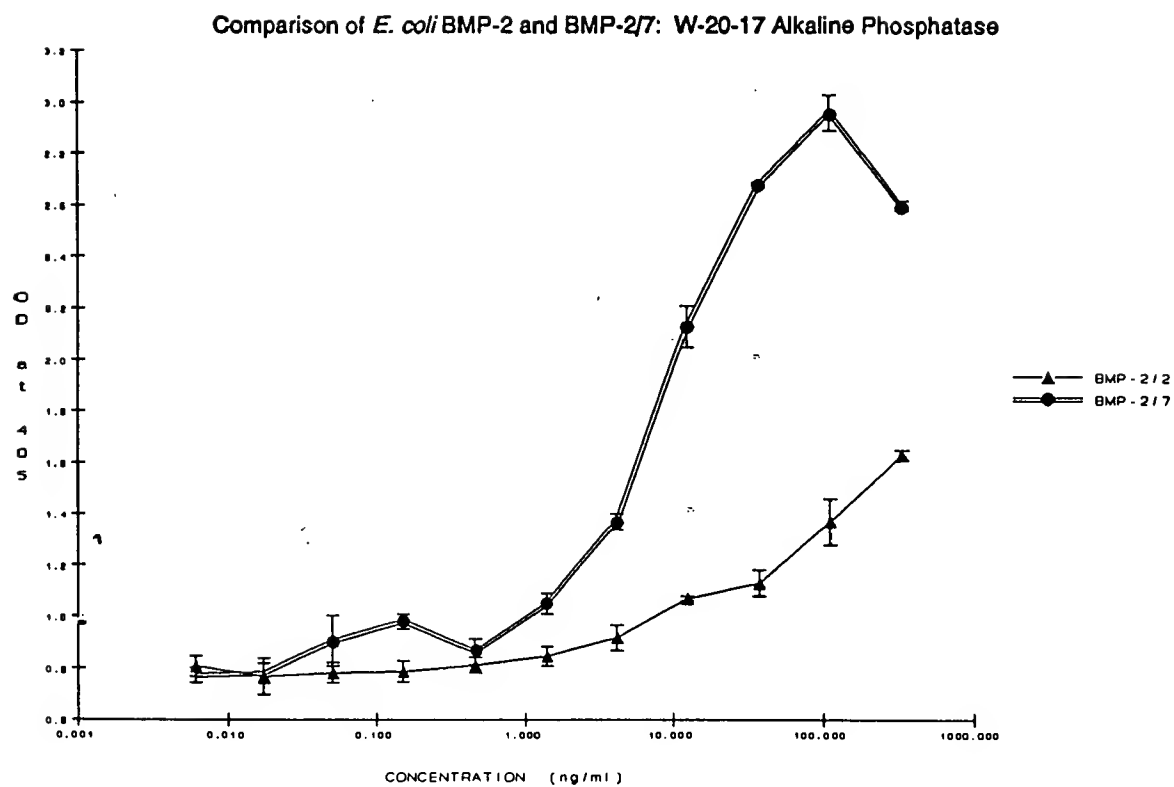


FIGURE 11

10 20 30 40 50 60 70
 AGATCTTGAA AACACCOGGG CCACACAAGC OGOGAOCCTAC AGCTCTTTCT CAGOGTTGGA GTGGACAAGG

80 90 100 110 120 130 140
 OGCCCGCAGC GOOCTGOGOG GGTGAGGTGC GGCAGCTGC TGGGGAAGAG CCCAOCCTGTC AGGCTGOGCT

150 160 170 180 190 200 210
 GGGTCAGOGC AGCAAGTGGG GCTGGCOGCT ATCTOGCTGC ACCOOGGOGC GTCCOOGGGCT COGTGOGCC

220 230 240 250 260 270 280
 TOGCCCCAGC TGGTTTGAG TTCAACCTC GGCTCOGOOG COGGCTOCTT GOGCTTGG AGTGTCCGC

290 300 310 320 (1) 335
 AGOGAOCGOG GGAGOOAGC OGOOGOGGG GTAOCTAGCC ATG GCT GGG GOG AGC AGG CTG CTC
 MET Ala Gly Ala Ser Arg Leu Leu

350 365 380 395
 TTT CTG TGG CTG GGC TGC TTC TGC GTG AGC CTG GCG CAG GGA GAG AGA COG AAG CCA
 Phe Leu Trp Leu Gly Cys Phe Cys Val Ser Leu Ala Gln Gly Glu Arg Pro Lys Pro

410 425 440 455
 CGT TTC COG GAG CTC OGC AAA GCT GTG CCA GGT GAC OGC ACG GCA GGT GGT GGC COG
 Pro Phe Pro Glu Leu Arg Lys Ala Val Pro Gly Asp Arg Thr Ala Gly Gly Gly Pro

470 485 500 515
 GAC TOC GAG CTG CAG COG CAA GAC AAG GTC TCT GAA CAC ATG CTG OGG CTC TAT GAC
 Asp Ser Glu Leu Gln Pro Gln Asp Lys Val Ser Glu His MET Leu Arg Leu Tyr Asp

530 545 560
 AGG TAC AGC ACG GTC CAG GCG GCC OGG ACA COG GGC TOC CTG GAG GGA GGC TOG CAG
 Arg Tyr Ser Thr Val Gln Ala Ala Arg Thr Pro Gly Ser Leu Glu Gly Gly Ser Gln

575 590 605 620
 CCC TGG OGC OCT OGG CTC CTG OGC GAA GGC AAC ACG GTC OGC AGC TTT OGG GCG GCA
 Pro Trp Arg Pro Arg Leu Leu Arg Glu Gly Asn Thr Val Arg Ser Phe Arg Ala Ala

635 650 665 680
 GCA GCA GAA ACT CTT GAA AGA AAA GGA CTG TAT ATC TTC AAT CTG ACA TOG CTA ACC
 Ala Ala Glu Thr Leu Glu Arg Lys Gly Leu Tyr Ile Phe Asn Leu Thr Ser Leu Thr

695 710 725 740
 AAG TCT GAA AAC ATT TTG TCT GCC ACA CTG TAT TTC TGT ATT GGA GAG CTA GGA AAC
 Lys Ser Glu Asn Ile Leu Ser Ala Thr Leu Tyr Phe Cys Ile Gly Glu Leu Gly Asn

FIGURE 11 (Continued)

755	770	785	800
ATC AGC CTG AGT TGT OCA GTG TCT GGA GGA TGC TOC CAT CAT GCT CAG AGG AAA CAC			
Ile Ser Leu Ser Cys Pro Val Ser Gly Gly Cys Ser His His Ala Gln Arg Lys His			
815	830	845	
ATT CAG ATT GAT CTT TCT GCA TGG ACC CTC AAA TTC AGC AGA AAC CAA AGT CAA CTC			
Ile Gln Ile Asp Leu Ser Ala Trp Thr Leu Lys Phe Ser Arg Asn Gln Ser Gln Leu			
860	875	890	905
CTT GGC CAT CTG TCA GTG GAT ATG GCC AAA TCT CAT OGA GAT ATT ATG TCC TGG CTG			
Leu Gly His Leu Ser Val Asp MET Ala Lys Ser His Arg Asp Ile MET Ser Trp Leu			
920	935	950	965
TCT AAA GAT ATC ACT CAA TTC TTG AGG AAG GCC AAA GAA AAT GAA GAG TTC CTC ATA			
Ser Lys Asp Ile Thr Gln Phe Leu Arg Lys Ala Lys Glu Asn Glu Glu Phe Leu Ile			
980	995	1010	1025
GGA TTT AAC ATT ACG TOC AAG GGA OGC CAG CTG OCA AAG AGG AGG TTA OCT TTT CCA			
Gly Phe Asn Ile Thr Ser Lys Gly Arg Gln Leu Pro Lys Arg Arg Leu Pro Phe Pro			
1040	1055	1070	1085
GAG OCT TAT ATC TTG GTA TAT GCC AAT GAT GOC GOC ATT TCT GAG OCA GAA AGT GTG			
Glu Pro Tyr Ile Leu Val Tyr Ala Asn Asp Ala Ala Ile Ser Glu Pro Glu Ser Val			
1100	1115	1130	
GTA TCA AGC TTA CAG GGA CAC OGG AAT TTT CCC ACT GGA ACT GTT CCC AAA TGG GAT			
Val Ser Ser Leu Gln Gly His Arg Asn Phe Pro Thr Gly Thr Val Pro Lys Trp Asp			
1145	1160	1175	1190
AGC CAC ATC AGA GCT GCC CTT TOC ATT GAG OGG AGG AAG AAG OGC TCT ACT GGG GTC			
Ser His Ile Arg Ala Ala Leu Ser Ile Glu Arg Arg Lys Lys Arg Ser Thr Gly Val			
1205	1220	1235	1250
TTG CTG CCT CTG CAG AAC AAC GAG CTT CCT GGG GCA GAA TAC CAG TAT AAA AAG GAT			
Leu Leu Pro Leu Gln Asn Asn Glu Leu Pro Gly Ala Glu Tyr Gln Tyr Lys Lys Asp			
1265	1280	1295	1310
GAG GTG TGG GAG GAG AGA AAG CCT TAC AAG ACC CTT CAG GCT CAG GCC OCT GAA AAG			
Glu Val Trp Glu Glu Arg Lys Pro Tyr Lys Thr Leu Gln Ala Gln Ala Pro Glu Lys			
1325	1340	1355	1370
AGT AAG AAT AAA AAG AAA CAG AGA AAG GGG CCT CAT OGG AAG AGC CAG ACG CTC CAA			
Ser Lys Asn Lys Lys Lys Gln Arg Lys Gly Pro His Arg Lys Ser Gln Thr Leu Gln			
1385	1400	1415	
TTT GAT GAG CAG ACC CTG AAA AAG GCA AGG AGA AAG CAG TGG ATT GAA CCT OGG AAT			
Phe Asp Glu Gln Thr Leu Lys Lys Ala Arg Arg Lys Gln Trp Ile Glu Pro Arg Asn			

